caBIG cancer Biomedical Informatics Grid

Integrative Cancer Research Special Interest Group Teleconference

Pathways SIG Meeting Minutes

Date, Time & Location:	July 6, 2004 1:00 – 2:00 EDT
Attendees:	Cathy Wu – Georgetown Brain Pittman – The Institute for Cancer Prevention Gary Bader – Sloan Vincent Yau – Oregon Health David Jewell – Dartmouth David Fenstermacher – Penn Rakesh Nagarajan – Wash U David Kane – SRA/NCI Carl Schaefer - NCI Claire Zhu – BAH Juli Klemm - BAH
Application Presentations	**BioPAX** Gary Bader (Sloan) gave a presentation of BioPAX. The slides can be downloaded from: http://ncicbforums.nci.nih.gov/forums/cabigforum/lfs/icrlfs/SIGs/pathways. BioPAX Q & A How does BioPAX deal with similar concepts having different meanings? (David Kane) - This is a problem of semantic mapping. BioPAX is initially focused on syntactic mapping. Detailed documentations will be provided for the mapping. Are there tools for creating BioPAX compatible pathway representations? (David Kane) - Such tools are not yet available. Is there plan for standardizing pathway names? (Cathy Wu) - There is someone at WIT looking into this, but there is not anything available for general use. Is there a publication on BioPAX? (Juli) - A publication is in preparation. Note that the documentation available on the website is very detailed. What is timeframe for release of Level 2 BioPAX? (Juli) - The goal is to have a draft version completed by the end of the summer. Level 2 BioPAX will support PSI and other higher-level interactions. Gene regulatory networks are slated for Level 3. **PIR** Cathy Wu (Georgetown) gave a presentation of PIR. The slides will be available for download from: http://ncicbforums.nci.nih.gov/forums/cabigforum/lfs/icrlfs/SIGs/pathways. PIR Q & A What is the rule for inferring pathways based on orthologous relationships? (Juli) - The parameter currently used is 50% identity over 80% of the length, But this can

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be adjusted/specified according to user preference.

How is functional association determined? (Gary Bader)

- Functional associations between genes are determined based on existing information in the databases. Predicted results are not yet incorporated.

To use iProXpress, is it correct that a user must perform gene expression analysis outside of the database? (Juli)

- Correct. iProXpress is best used when a user already have a list of genes from clustering analysis and wants to know more about the genes.

Is iProXpress scalable for analysis of, say, 30,000 genes? Is the result exportable to Excel? (David)

- Yes, analysis results are exportable to Excel. Analysis of large number of genes is doable, but it may take some time. A better way to do it is to submit the list of genes, and have the results sent back as an interactive web page.

Is it the intent of PIR to remain a local server, or can it be implemented at cancer centers?

- We can develop a package that can be distributed and implemented at the cancer centers.

Other Items Discussed

- Next meeting is August 3, 1:00PM ET.
- Please respond with preferred dates for the ICR face-to-face meeting.

Action Items:

Name Responsible	Action Item	Date Due	Notes
Juli Klemm	Post slides from presentations to the forum	7/7/04	
Juli Klemm	Distribute meeting minutes	7/9/04	
Juli Klemm	Follow up on presentations for next meeting.	7/16/04	